

		10	20	
1	T	G	P	G
1	H			
		30	40	
21	H	C	E	P
3				
		50	60	
41	A	D	A	R
8				
		70	80	
49	H	F	C	D
24	I	F	H	N
		90	100	
64	L	S	Q	Y
44	A	G	R	Y
		110	120	
84	T	M	A	T
64	R	L	A	T
		130	140	
104	A	G	U	L
84	A	G	I	M
		150	160	
124	S	S	G	V
104	G	F	G	K
		170	180	
144	D	V	F	C
124	D	A	Y	C
		190	200	
159	V	Q	Y	V
144	R	I	F	K
		210	220	
174				
164	H	I	R	L
		230	240	
182				
184	H	D	P	S
		250	260	
197	A	P	G	R
204				
		270	280	
217	V	P		
206	V	S	R	Y
		290	300	
235	E	H	H	L
226	T	L	F	F
		310	320	
255	L	Q	T	R
236	T	A	G	S
		330	340	
275	T	E	T	R
249	P	A	S	F
		350	360	
295	S	I	T	H
263	S	N	K	F
		370	380	
315	H	T	G	L
270				
		390		
335	L	A	A	Y
270				

Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

Percent Identity			
Divergence		1	2
	1		31.6
	2	100.0	
		1	2
BM-HABP Fig.4.PRO			
TSG-6.PRO			



# Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

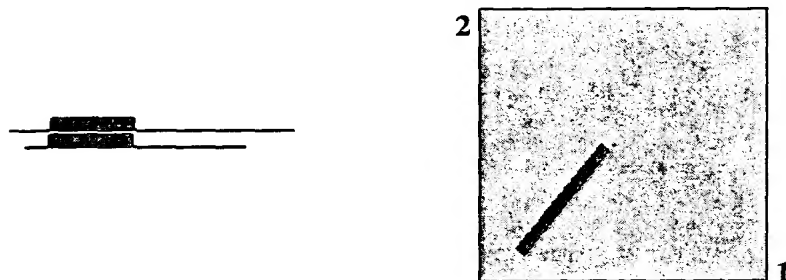
Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.1.2 [Oct-19-2000]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**  
 x\_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☒ Align

Sequence 1 lc1lsèq\_1 Length 353 (1 .. 353)

Sequence 2 lc1lsèq\_2 Length 275 (1 .. 275)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 107 bits (264), Expect = 5e-21  
 Identities = 45/104 (43%), Positives = 61/104 (58%)

Query: 52 DTTVGVFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGR 111  
 + GV+H + G+YKLT+ +A+ C E +ATY QL +K +H+C+AGW+ GR  
 Sbjct: 32 EQAAGVYHREARAGRYKLTAEAKAVCEFEGRRLATYKQLEAARKIGFHVCAAGWMAKGR 91

Query: 112 VAYPTAFASQNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVCNC 155  
 V YP NCG G GI+DYG R N+SE WD +CY C  
 Sbjct: 92 VGYPVIVKPGPNCGFGKTGIIDYGIRLNRSERWDAYCYNPHAKEC 135

CPU time: 0.15 user secs. 0.03 sys. secs 0.18 total secs.

Gapped

Lambda	K	H
0.321	0.138	0.429

Gapped

Lambda	K	H
0.270	0.0470	0.230

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 748

Number of Sequences: 0

Number of extensions: 55

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 353  
length of database: 3,171,650,076  
effective HSP length: 58  
effective length of query: 295  
effective length of database: 3,171,650,018  
effective search space: 935636755310  
effective search space used: 935636755310  
T: 9  
A: 40  
X1: 16 ( 7.4 bits)  
X2: 128 (49.9 bits)  
X3: 128 (49.9 bits)  
S1: 41 (21.9 bits)  
S2: 83 (36.7 bits)

**EXHIBIT C**

56 GVFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLC SAGWLETGRVAYP -SEQ ID NO:11  
|||||  
1063 GVFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYAQKAKYHLC SAGWLETGRVAYP -human HARE

115 TAFASQNCGSGVVGIVDYGPRPNKSEMWDVFCYR 149  
|||||  
1122 TAFASQNCGSGVVGIVDYGPRPNKSEMWDVFCYR 1156

# CURRENT PROTOCOLS IN MOLECULAR BIOLOGY

VOLUME 1

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CORE 13 (536)

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*Library of Congress Cataloging in Publication Data:*

Current protocols in molecular biology. 3 vols.

1. Molecular biology—Technique. 2. Molecular biology—Laboratory manuals. I. Annabel, Frederick M.

QH506.C87 1987 574.873028 87-21033

ISBN 0-471-50338-X

Printed in the United States of America

20 19 18 17 16 15 14 13

- 1c. *Harsh treatment:* Pour several hundred milliliters of boiling 0.1% SDS onto the membrane. Cool to room temperature.

*If a membrane is to be reprobed, it must not be allowed to dry out between hybridization and stripping. If it becomes dry, the probe may bind to the matrix.*

2. Place membrane on a sheet of dry Whatman 3MM filter paper and blot excess liquid with a second sheet. Wrap the membrane in plastic wrap and set up an autoradiograph.

*If signal is still seen after autoradiography, rewash using harsher conditions.*

3. The membrane can now be rehybridized. Alternatively, it can be dried and stored for later use.

*Membranes can be stored dry between Whatman 3MM paper for several months at room temperature. For long-term storage, place the membranes in a desiccator at room temperature or 4°C.*

## REAGENTS AND SOLUTIONS

### *Aqueous prehybridization/hybridization (APH) solution*

5× SSC (APPENDIX 2)

5× Denhardt solution (APPENDIX 2)

1% (w/v) SDS

Add 100 µg/ml denatured salmon sperm DNA (see below) just before use

*Alternatives to Denhardt solution and denatured salmon sperm DNA as blocking agents are listed in Table 2.10.5 (see discussion in critical parameters).*

### *Denatured salmon sperm DNA*

Dissolve 10 mg Sigma type III salmon sperm DNA (sodium salt) in 1 ml water. Pass vigorously through a 17-G needle 20 times to shear the DNA. Place in a boiling water bath for 10 min, then chill. Use immediately or store at -20°C in small aliquots. If stored, reheat to 100°C for 5 min and chill on ice immediately before using.

### *Formamide prehybridization/hybridization (FPH) solution*

5× SSC (APPENDIX 2)

5× Denhardt solution (APPENDIX 2)

50% (w/v) formamide

1% (w/v) SDS

Add 100 µg/ml denatured salmon sperm DNA (see above) just before use

*Alternatives to Denhardt solution and denatured salmon sperm DNA as blocking agents are listed in Table 2.10.5 (see discussion in critical parameters).*

*Commercial formamide is usually satisfactory for use. If the liquid has a yellow color, deionize as follows: add 5 g of mixed-bed ion-exchange resin [e.g., Bio-Rad AG 501-X8 or 501-X8(D) resins] per 100 ml formamide, stir at room temperature for 1 hr, and filter through Whatman no. 1 paper.*

*CAUTION: Formamide is a teratogen. Handle with care.*

### *Labeling buffer*

200 mM Tris-Cl, pH 7.5

30 mM MgCl<sub>2</sub>

10 mM spermidine

### *Mild stripping solution*

5 mM Tris-Cl, pH 8.0

2 mM EDTA

0.1× Denhardt solution (APPENDIX 2)



**SDS electrophoresis buffer, 5×**

15.1 g Tris base

72.0 g glycine

5.0 g SDS

H<sub>2</sub>O to 1000 ml

Dilute to 1× or 2× for working solution, as appropriate

Do not adjust the pH of the stock solution, as the solution is pH 8.3 when diluted. Store at 0° to 4° C until use (up to 1 month).

**SED (standard enzyme diluent)**

20 mM Tris-Cl, pH 7.5

500 µg/ml bovine serum albumin (Pentax Fraction V)

10 mM 2-mercaptoethanol

Store up to 1 month at 4° C

**Sodium acetate, 3 M**

Dissolve 408 g sodium acetate-3H<sub>2</sub>O in 800 ml H<sub>2</sub>O

Add H<sub>2</sub>O to 1 liter

Adjust pH to 4.8 or 5.2 (as desired) with 3 M acetic acid

**Sodium acetate buffer, 0.1 M**

Solution A: 11.55 ml glacial acetic acid/liter (0.2 M).

Solution B: 27.2 g sodium acetate (NaC<sub>2</sub>H<sub>3</sub>O<sub>2</sub>·3H<sub>2</sub>O)/liter (0.2 M).

Referring to Table A.2.2 for desired pH, mix the indicated volumes of solutions A and B, then dilute with H<sub>2</sub>O to 100 ml. (See Potassium acetate buffer recipe for further details.)

**Sodium phosphate buffer, 0.1 M**

Solution A: 27.6 g NaH<sub>2</sub>PO<sub>4</sub>·H<sub>2</sub>O per liter (0.2 M).

Solution B: 53.65 g Na<sub>2</sub>HPO<sub>4</sub>·7H<sub>2</sub>O per liter (0.2 M).

Referring to Table A.2.3 for desired pH, mix the indicated volumes of solutions A and B, then dilute with H<sub>2</sub>O to 200 ml. (See Potassium phosphate buffer recipe for further details.)

**SSC (sodium chloride/sodium citrate), 20×**

3 M NaCl (175 g/liter)

0.3 M Na<sub>3</sub>citrate-2H<sub>2</sub>O (88 g/liter)

Adjust pH to 7.0 with 1 M HCl

**STE buffer**

10 mM Tris-Cl, pH 7.5

10 mM NaCl

1 mM EDTA, pH 8.0

**TAE (Tris/acetate/EDTA) electrophoresis buffer**

50× stock solution:

242 g Tris base

57.1 ml glacial acetic acid

37.2 g Na<sub>2</sub>EDTA-2H<sub>2</sub>O

H<sub>2</sub>O to 1 liter

Working solution, pH ~8.5:

40 mM Tris-acetate

2 mM Na<sub>2</sub>EDTA-2H<sub>2</sub>O

**TBE (Tris/borate/EDTA) electrophoresis buffer**

10× stock solution, 1 liter:

108 g Tris base (890 mM)

55 g boric acid (890 mM)

40 ml 0.5 M EDTA, pH 8.0 (20 mM)